

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma  
Yasuaki Ito  
Ryo Fujii

1,2390  
(ii) TITLE OF INVENTION: G Protein Coupled Receptor Protein,  
Production, And Use Thereof

(iii) NUMBER OF SEQUENCES: 61

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: BOSTON  
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(E) COUNTRY: USA  
(F) ZIP: 02209

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

E1  
(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/461,436  
(B) FILING DATE: 14-DECEMBER-1999  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/513,974  
(B) FILING DATE: 14-SEP-1995

(A) APPLICATION NUMBER: PCT/JP95/01599  
(B) FILING DATE: 10-AUG-1995

(A) APPLICATION NUMBER: 7-093989  
(B) FILING DATE: 19-APR-1995

(A) APPLICATION NUMBER: 7-057186  
(B) FILING DATE: 16-MAR-1995

(A) APPLICATION NUMBER: 7-007177  
(B) FILING DATE: 20-JAN-1995

(A) APPLICATION NUMBER: 6-326611  
(B) FILING DATE: 28-DEC-1994

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(A) APPLICATION NUMBER: 6-189273

(B) FILING DATE: 11-AUG-1994

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(B) FILING DATE: 11-AUG-1994

(viii) ATTORNEY/AGENT INFORMATION

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(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D) OTHER INFORMATION: /note= N is A, G, C, or T; S is G or C;  
M is A or C; Y is T or C."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGTGGSCMTS STGGGCAACN YCCTG

25

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D)OTHER INFORMATION:/note= N is A, G, C, or T; W is A or T;  
R is A or G; K is G or T."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GTNGWRRGGC ANCCAGCAGA KGGCAAA 27

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D)OTHER INFORMATION:/note= N is inosine; S is G or C;  
Y is C or T; M is A or C; R is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCGCSGCYM TNRGYATGGA YCGNTAT 27

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D)OTHER INFORMATION:/note= N is inosine; R is A or G;  
W is T or A; S is G or C; M is A or C."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CATGTRGWAG GGAANCCAGS AMANRRARRAA 30

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27  
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:  
(D) OTHER INFORMATION: /note= N is inosine; Y is C or T;  
R is A or G; S is G or C; M is A or C; V is A, C or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTGACYGYTC TNRSNRYTGA CMGVTAC 27

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

E1 (ix) FEATURE:  
(D) OTHER INFORMATION: /note= N is inosine; Y is C or T;  
R is A or G; S is G or C; M is A or C; V is A, C or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTGACYGYTC TNRSNRYTGA CMGVTAT 27

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:  
(D) OTHER INFORMATION: /note= N is inosine; S is G or C;  
Y is C or T; M is A or C; R is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTCGCSGCMY TNRGYATGGA YCGNTAC 27

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D) OTHER INFORMATION: /note= N is inosine; R is A or G;  
S is G or C; Y is C or T."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GATGTGRTAR GGSRNCCAAC AGANGRYAAA 30

E1  
(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D) OTHER INFORMATION: /note= N is inosine; R is A or G;  
S is G or C; Y is C or T."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GATGTGRTAR GGSRNCCAAC AGANGRYGAA 30

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27

(B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
 (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:  
 (D) OTHER INFORMATION: /note= N is inosine; S is G or C;  
 Y is C or T; W is A or T; H is A, C or T."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GYCACCAACN WSTTCATCCT SWNHCTG 27

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
 (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:  
 (D) OTHER INFORMATION: /note= N is inosine; R is A or G;  
 S is G or C."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ASNSANRAAG SARTAGANGA NRGGRTT 27

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
 (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:  
 (D) OTHER INFORMATION: /note= N is inosine; S is G or C;  
 K is G or T; M is A or C."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TGNTSSTKMT NGSNGTKGTN GGNA 25

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D) OTHER INFORMATION: /note= N is inosine; Y is C or T;  
K is G or T; W is A or T."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AYCKGTAYCK GTCCANKGWN ATKGC 25

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D) OTHER INFORMATION: /note= N is inosine; K is G or T;  
S is G or C; Y is C or T; R is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CATKKCCSTG GASAGNTAYN TRGC 24

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24  
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:  
(D) OTHER INFORMATION: /note= N is inosine; W is A or T;  
S is G or C; K is G or T; R is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GWGGGGSAKC CAGCASANGG CRAA

24

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:  
(D) OTHER INFORMATION: /note= N at position 6, 9, 10 & 12 = inosine;  
N at position 15 = A, G, C, or T; R is A or G; Y is C or T."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ARYYTNGCNN TNGCNGAY

18

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:  
(D) OTHER INFORMATION: /note= N at position 1, 4, & 6 = inosine;  
N at position 13, 15, 16 & 18 = A, G, C, or T; R is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:



NGGNANCCAR CANANNRNRA A

21

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

## (ix) FEATURE:

- (D) OTHER INFORMATION: /note= N is inosine; S is G or C; R is A or G;  
W is A or T; M is A or C."

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCTSNTNRN SATGWSTGTG GANMGNT

27

## E1 (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

## (ix) FEATURE:

- (D) OTHER INFORMATION: /note= N is inosine, W is A or T,  
S is G or C, M is A or C, Y is C or T, R is A or G."

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GAWSNTGMYN ANRTGGWAGG GNANCCA

27

## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TAGTGTGTGG AGTCGTGTGG CTGGCTG 27

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

AGTCTTTGCT GCCACAGGCA TCCAGCG 27

E1  
(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CAAGCCAGTA AGGCTATGAA GGCAGCAAG 30

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ACAGGACCTG CTGGGCCATC CTGGCGACAC A 31

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91  
(B) TYPE: Amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn  
1 5 10 15  
Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala  
20 25 30  
Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val  
35 40 45  
Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr  
50 55 60  
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr  
65 70 75 80  
Val Val Leu Val His Pro Leu Arg Arg Arg Ile  
85 90

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59  
(B) TYPE: Amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu  
1 5 10 15  
Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly

	20		25		30									
Cys	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg
	35						40					45		
Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val				
	50					55								

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

E1

Met	Ala	Ser	Ser	Thr	Thr	Arg	Gly	Pro	Arg	Val	Ser	Asp	Leu	Phe	Ser
1				5					10					15	
Gly	Leu	Pro	Pro	Ala	Val	Thr	Thr	Pro	Ala	Asn	Gln	Ser	Ala	Glu	Ala
			20					25					30		
Ser	Ala	Gly	Asn	Gly	Ser	Val	Ala	Gly	Ala	Asp	Ala	Pro	Ala	Val	Thr
	35						40					45			
Pro	Phe	Gln	Ser	Leu	Gln	Leu	Val	His	Gln	Leu	Lys	Gly	Leu	Ile	Val
	50				55					60					
Leu	Leu	Tyr	Ser	Val	Val	Val	Val	Val	Gly	Leu	Val	Gly	Asn	Cys	Leu
65				70					75					80	
Leu	Val	Leu	Val	Ile	Ala	Arg	Val	Arg	Arg	Leu	His	Asn	Val	Thr	Asn
			85					90						95	
Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu	Met	Cys	Thr	Ala
		100					105						110		
Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly	Trp	Val
	115					120						125			
Phe	Gly	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Pro	Val	Thr
	130				135						140				
Val	Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr
145				150					155						160
Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser
			165				170						175		
Ala	Tyr	Ala	Val	Leu	Ala	Ile	Trp	Ala	Leu	Ser	Ala	Val	Leu	Ala	Leu

E1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu Tyr Asn Val Thr Asn  
1 5 10 15

Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala

E1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser  
1 5 10 15

Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu  
20 25 30

Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val

35	40	45
Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Ile		
50	55	60
Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala		
65	70	75
Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val		
85	90	95
Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg		
100	105	110
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val		
115	120	125

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGCACAACG TGACGAACTT CCTCATCGGC	60
AACCTGGCCT TGTCCGACGT GCTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT	120
GCCTTCGAGC CACGCGGCTG GGTGTTCTGGC GCGGGCCTGT GCCACCTGGT CTTCTTCCTG	180
CAGCCGGTCA CCGTCTATGT GTCGGTGTTC ACGCTCACCA CCATCGCAGT GGACCGGTAC	240
GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATC	273

## (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGCCTGCTGC TGGTCACCTA CCTGCTCCCT CTGCTGGTCA TCCTCCTGTC TTACGTCCGG	60
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GTGTCAGTGA AGCTCCGCAA CCGCGTGGTG CCGGGCTGCG TGACCCAGAG CCAGGCCGAC 120  
 TGGGACCGCG CTCGGCGCCG GCGCACCTTC TGCTTGCTGG TGGTGGTCGT GGTGGTG 177

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

E1  
 ATGGCCTCAT CGACCACTCG GGGCCCCAGG GTTCTGACT TATTTTCTGG GCTGCCGCCG 60  
 GCGGTCACAA CTCCCGCCAA CCAGAGCGCA GAGGCCTCGG CGGGCAACGG GTCGGTGGCT 120  
 GGCGCGGACG CTCCAGCCGT CACGCCCTTC CAGAGCCTGC AGCTGGTGCA TCAGCTGAAG 180  
 GGGCTGATCG TGCTGCTCTA CAGCGTCGTG GTGGTCGTGG GGCTGGTGGG CAACTGCCTG 240  
 CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGCACAACG TGACGAACTT CCTCATCGGC 300  
 AACCTGGCCT TGTCCGACGT GCTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT 360  
 GCCTTCGAGC CACGCGGCTG GGTGTTCCGG GCGGCCTGT GCCACCTGGT CTTCTTCCTG 420  
 CAGCCGGTCA CCGTCTATGT GTCGGTGTTT ACGCTACCA CCATCGCAGT GGACCGCTAC 480  
 GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATCTCGCTGC GCCTCAGCGC CTACGCTGTG 540  
 CTGGCCATCT GGGCGCTGTC CGCGGTGCTG GCGCTGCCCC CCGCCGTGCA CACCTATCAC 600  
 GTGGAGCTCA AGCCGCACGA CGTGCGCCTC TGCGAGGAGT TCTGGGGCTC CCAGGAGCGC 660  
 CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACCTGCTCCC TCTGCTGGTC 720  
 ATCCTCCTGT CTTACGTCCG GGTGTCAGTG AAGCTCCGCA ACCGCGTGGT GCCGGGCTGC 780  
 GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGCACCTT CTGCTTGCTG 840  
 GTGGTGGTCG TGGTGGTGTT CGCCGTCTGC TGGCTGCCGC TGACAGTCTT CAACCTGCTG 900  
 CGGGACCTCG ACCCCACGC CATCGACCCT TACGCCTTTG GGCTGGTGCA GCTGCTCTGC 960  
 CACTGGCTCG CCATGAGTTC GGCCTGCTAC AACCCTTCA TCTACGCTG GCTGCACGAC 1020  
 AGCTTCCGCG AGGAGCTGCG CAAACTGTTG GTCGCTTGGC CCCGCAAGAT AGCCCCCAT 1080  
 GGCCAGAATA TGACCGTCAG CGTGGTCATC 1110



## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGTACAACG TGACGAATTT CCTCATCGGC 60  
 AACCTGGCCT TGTCCGACGT GTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT 120  
 GCCTTCGAGC CACGCGGCTG GGTGTTCTGGC GCGGCCTGT GCCACCTGGT CTTCTTCCTG 180  
 CAGGCGGTCA CCGTCTATGT GTCGGTGTTC ACGCTACCA CCATCGCAGT GGACCGCTAC 240  
 GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATCTCGCTGC GCCTCAGCGC CTACGCTGTG 300  
 CTGGCCATCT GGGTGCTGTC CGCGGTGCTG GCGCTGCCCCG CCGCCGTGCA CACCTATCAC 360  
 GTGGAGCTCA AGCCGCACGA CGTGCGCCTC TGCGAGGAGT TCTGGGGCTC CCAGGAGCGC 420  
 CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACCTGCTCCC TCTGCTGGTC 480  
 ATCCTCCTGT CTTACGCCCCG GGTGTCAGTG AAGCTCCGCA ACCGCGTGGT GCCGGGCCGC 540  
 GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGCACCTT CTGCTTGCTG 600  
 GTGGTGGTGCG TGGTGGTG 618

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTGGTTCTGG TGCACCCGCT ACGTCGGCGC ATTTCACTGA GGCTCAGCGC CTACGCGGTG 60  
 CTGGGCATCT GGGCTCTATC TGCAGTGCTG GCGCTGCCGG CCGCGGTGCA CACCTACCAT 120

```

GTGGAGCTCA AGCCCCACGA CGTGAGCCTC TGCGAGGAGT TCTGGGGCTC GCAGGAGCGC      180
CAACGCCAGA TCTACGCCTG GGGGCTGCTT CTGGGCACCT ATTTGCTCCC CCTGCTGGCC      240
ATCCTCCTGT CTTACGTACG GGTGTCAGTG AAGCTGAGGA ACCGCGTGGT GCCTGGCAGC      300
GTGACCCAGA GTCAAGCTGA CTGGGACCGA GCGCGTCGCC GCCGCACTTT CTGTCTGCTG      360
GTGGTGGTGG TGGTAGTG                                     378

```

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

E1

```

Val Cys His Val Ile Phe Lys Asn Gln Arg Met His Ser Ala Thr Ser
 1             5             10             15
Leu Phe Ile Val Asn Leu Ala Val Ala Asp Ile Met Ile Thr Leu Ile
      20             25             30
Asn Thr Pro Phe Thr Leu Val Arg Phe Val Asn Ser Thr Trp Ile Phe
      35             40             45
Gly Lys Gly Met Cys His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu
      50             55             60
His Val Ser Ala Leu Thr
      65             70

```

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

Glu Pro Ala Asp Leu Phe Trp Lys Asn Leu Asp Leu Pro Thr Phe Ile
 1             5             10             15

```

Leu Leu Asn Ile Leu Pro Leu Leu Ile Ile Ser Val Ala Tyr Val Arg  
                   20                                  25                                  30  
 Val Thr Lys Lys Leu Trp Leu Cys Asn Met Ile Val Asp Val Thr Thr  
                   35                                  40                                  45  
 Glu Gln Tyr Phe Ala Leu Arg Pro Lys Lys Lys Lys Thr Ile Lys Met  
                   50                                  55                                  60  
 Leu Met Leu Val Val Val Leu  
 65                                  70

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTCTGTCATG TCATCTTCAA GAACCAGCGA ATGCACTCGG CCACCAGCCT CTTCATCGTC 60  
 AACCTGGCAG TTGCCGACAT AATGATCACG CTGCTCAACA CCCCCTTCAC TTTGGTTTCGC 120  
 TTTGTGAACA GCACATGGAT ATTTGGGAAG GGCATGTGCC ATGTCAGCCG CTTTGCCCAG 180  
 TACTGCTCAC TGCACGTCTC AGCACTGACA 210

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 213 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAGCCAGCTG ACCTCTTCTG GAAGAACCTG GACTTGCCCA CCTTCATCCT GCTCAACATC 60  
 CTGCCCCTCC TCATCATCTC TGTGGCCTAC GTTCGTGTGA CCAAGAAACT GTGGCTGTGT 120  
 AATATGATTG TCGATGTGAC CACAGAGCAG TACTTTGCCC TGCGGCCCAA AAAGAAGAAG 180  
 ACCATCAAGA TGTTGATGCT GGTGGTAGTC CTC 213

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ala Ser Trp His Lys Arg Gly Gly Arg Arg Ala Ala Trp Val Val Cys  
 1 5 10 15

Gly Val Val Trp Leu Ala Val Thr Ala Gln Cys Leu Pro Thr Ala Val  
 20 25 30

Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val Cys Tyr Asp Leu  
 35 40 45

Ser Pro Pro Ile Leu Ser Thr Arg Tyr Leu Pro Tyr Gly Met Ala Leu  
 50 55 60

Thr Val Ile Gly Phe Leu Leu Pro Phe Ile Ala Leu Leu Ala Cys Tyr  
 65 70 75 80

Cys Arg Met Ala Arg Arg Leu Cys Arg Gln Asp Gly Pro Ala Gly Pro  
 85 90 95

Val Ala Gln Glu Arg Arg Ser Lys Ala Ala Arg Met Ala Val Val Val  
 100 105 110

Ala Ala Val  
 115

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Glu Gln Asp Asn Gly Thr Ile Gln Ala Pro Gly Leu Pro Pro Thr  
 1 5 10 15

Thr Cys Val Tyr Arg Glu Asp Phe Lys Arg Leu Leu Leu Thr Pro Val  
 20 25 30  
 Tyr Ser Val Val Leu Val Val Gly Leu Pro Leu Asn Ile Cys Val Ile  
 35 40 45  
 Ala Gln Ile Cys Ala Ser Arg Arg Thr Leu Thr Arg Ser Ala Val Tyr  
 50 55 60  
 Thr Leu Asn Leu Ala Leu Ala Asp Leu Met Tyr Ala Cys Ser Leu Pro  
 65 70 75 80  
 Leu Leu Ile Tyr Asn Tyr Ala Arg Gly Asp His Trp Pro Phe Gly Asp  
 85 90 95  
 Leu Ala Cys Arg Phe Val Arg Phe Leu Phe Tyr Ala Asn Leu His Gly  
 100 105 110  
 Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly Ile  
 115 120 125  
 Cys His Pro Leu Ala Ser Trp His Lys Arg Gly Gly Arg Arg Ala Ala  
 130 135 140  
 Trp Val Val Cys Gly Val Val Trp Leu Ala Val Thr Ala Gln Cys Leu  
 145 150 155 160  
 Pro Thr Ala Val Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val  
 165 170 175  
 Cys Tyr Asp Leu Ser Pro Pro Ile Leu Ser Thr Arg Tyr Leu Pro Tyr  
 180 185 190  
 Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ile Ala Leu  
 195 200 205  
 Leu Ala Cys Tyr Cys Arg Met Ala Arg Arg Leu Cys Arg Gln Asp Gly  
 210 215 220  
 Pro Ala Gly Pro Val Ala Gln Glu Arg Arg Ser Lys Ala Ala Arg Met  
 225 230 235 240  
 Ala Val Val Val Ala Ala Val Phe Ala Ile Ser Phe Leu Pro Phe His  
 245 250 255  
 Ile Thr Lys Thr Ala Tyr Leu Ala Val Arg Ser Thr Pro Gly Val Ser  
 260 265 270  
 Cys Pro Val Leu Glu Thr Phe Ala Ala Ala Tyr Lys Gly Thr Arg Pro  
 275 280 285  
 Phe Ala Ser Val Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe Thr  
 290 295 300  
 Gln Gln Lys Phe Arg Arg Gln Pro His Asp Leu Leu Gln Arg Leu Thr  
 305 310 315 320

E1

Ala Lys Trp Gln Arg Gln Arg Val  
325

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCTTCCTGGC ACAAGCGTGG AGGTCGCCGT GCTGCTTGGG TAGTGTGTGG AGTCGTGTGG 60  
 CTGGCTGTGA CAGCCCAGTG CCTGCCCACG GCAGTCTTTG CTGCCACAGG CATCCAGCGC 120  
 AACCGCACTG TGTGCTACGA CCTGAGCCCA CCCATCCTGT CTACTCGCTA CCTGCCCTAT 180  
 GGTATGGCCC TCACGGTCAT CGGCTTCTTG CTGCCCTTCA TAGCCTTACT GGCTTGTTAT 240  
 TGTCGCATGG CCCGCCGCCT GTGTCGCCAG GATGGCCCAG CAGGTCCTGT GGCCCAAGAG 300  
 CGGCGCAGCA AGGCGGCTCG TATGGCTGTG GTGGTGGCAG CTGTC 345

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 984 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGGAGCAGG ACAATGGCAC CATCCAGGCT CCAGGCTTGC CGCCCACCAC CTGCGTCTAC 60  
 CGTGAGGATT TCAAGCGACT GCTGCTAACC CCGGTATACT CGGTGGTGCT GGTGGTCGGC 120  
 CTGCCACTGA ACATCTGCGT CATTGCCCAG ATCTGCGCAT CCCGCCGGAC CCTGACCCGT 180  
 TCCGCTGTGT ACACCCTGAA CCTGGCACTG GCGGACCTGA TGTATGCCTG TTTACTACCC 240  
 CTACTTATCT ATAACCTACGC CAGAGGGGAC CACTGGCCCT TCGGAGACCT CGCCTGCCGC 300  
 TTTGTACGCT TCCTCTTCTA TGCCAATCTA CATGGCAGCA TCCTGTTTCT CACCTGCATT 360

```

AGCTTCCAGC GCTACCTGGG CATCTGCCAC CCCCTGGCTT CCTGGCACAA GCGTGGAGGT      420
CGCCGTGCTG CTTGGGTAGT GTGTGGAGTC GTGTGGCTGG CTGTGACAGC CCAGTGCCTG      480
CCCACGGCAG TCTTTGCTGC CACAGGCATC CAGCGCAACC GCACTGTGTG CTACGACCTG      540
AGCCCACCCA TCCTGTCTAC TCGCTACCTG CCCTATGGTA TGGCCCTCAC GGTCATCGGC      600
TTCTTGCTGC CCTTCATAGC CTTACTGGCT TGTTATTGTC GCATGGCCCG CCGCCTGTGT      660
CGCCAGGATG GCCCAGCAGG TCCTGTGGCC CAAGAGCGGC GCAGCAAGGC GGCTCGTATG      720
GCTGTGGTGG TGGCAGCTGT CTTTGCCATC AGCTTCCTGC CTTTCCACAT CACCAAGACA      780
GCCTACTTGG CTGTGCGCTC CACGCCCCGT GTCTCTTGCC CTGTGCTGGA GACCTTCGCT      840
GCTGCCTACA AAGGCACTCG GCCCTTCGCC AGTGTCAACA GTGTTCTGGA CCCATTCTC      900
TTCTACTTCA CACAACAGAA GTTCCGGCGG CAACCCACAG ATCTCTTACA GAGGCTCACA      960
GCCAAGTGGC AGAGGCAGAG AGTC                                             984

```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ala Ala Met Ser Val Asp Arg Tyr Val Ala Ile Val His Ser Arg Arg  
 1 5 10 15

Ser Ser Ser Leu Arg Val Ser Arg Asn Ala Leu Leu Gly Val Gly Phe  
 20 25 30

Ile Trp Ala Leu Ser Ile Ala Met Ala Ser Pro Val Ala Tyr His Gln  
 35 40 45

Arg Leu Phe His Arg Asp Ser Asn Gln Thr Phe Cys Trp Glu Gln Trp  
 50 55 60

Pro Asn Lys Leu His Lys Lys Ala Tyr Val Val Cys Thr Phe Val Phe  
 65 70 75 80

Gly Tyr Leu Leu Pro Leu Leu Leu Ile Cys Phe Cys Tyr Ala Lys Val  
 85 90 95

Leu Asn His Leu His Lys Lys Leu Lys Asn Met Ser Lys Lys Ser Glu

100	105	110
Ala Ser Lys Lys Lys Thr Ala Gln Thr Val Leu Val Val Val Val		
115	120	125

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

E1

GCCGCGATGT CTGTGGATCG CTACGTGGCC ATTGTGCACT CGCGGCGCTC CTCCTCCCTC	60
AGGGTGTCCC GCAACGCACT GCTGGGCGTG GGCTTCATCT GGGCGCTGTC CATCGCCATG	120
GCCTCGCCGG TGGCCTACCA CCAGCGTCTT TTCCATCGGG ACAGCAACCA GACCTTCTGC	180
TGGGAGCAGT GGCCCAACAA GCTCCACAAG AAGGCTTACG TGGTGTGCAC TTTCGTCTTT	240
GGGTACCTTC TGCCCTTACT GCTCATCTGC TTTTGCTATG CCAAGGTCCT TAATCATCTG	300
CATAAAAAGC TGAAAAACAT GTCAAAAAAG TCTGAAGCAT CCAAGAAAAA GACTGCACAG	360
ACCGTCCTGG TGGTCGTTGT AGTA	384

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Val Leu Trp Phe Phe Gly Phe Ser Ile Lys Arg Thr Pro Phe Ser Val	
1 5 10 15	
Tyr Phe Leu His Leu Ala Ser Ala Asp Gly Ala Tyr Leu Phe Ser Lys	
20 25 30	
Ala Val Phe Ser Leu Leu Asn Ala Gly Gly Phe Leu Gly Thr Phe Ala	
35 40 45	



His Tyr Val Arg Ser Val Ala Arg Val Leu Gly Leu Cys Ala Phe Val  
 50 55 60

Ala Gly Val Ser Leu Leu Pro  
 65 70

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GTGCTCTGGT TCTTCGGCTT CTCCATCAAG AGGACCCCTT TCTCCGTCTA CTCCTGCAC 60

CTGGCCAGCG CCGACGGCGC CTACCTCTTC AGCAAGGCCG TGTTCCTCCCT GCTGAACGCC 120

GGCGGCTTCC TGGGCACCTT CGCCCACTAT GTGCGCAGCG TGGCCCGGGT GCTGGGGCTC 180

TGCGCCTTCG TGGCGGGCGT GAGCCTCCTG CCGGC 215

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Glu Leu Ala Met Val Asn Leu Ser Glu Gly Asn Gly Ser Asp Pro  
 1 5 10 15

Glu Pro Pro Ala Pro Glu Ser Arg Pro Leu Phe Gly Ile Gly Val Glu  
 20 25 30

Asn Phe Ile Thr Leu Val Val Phe Gly Leu Ile Phe Ala Met Gly Val  
 35 40 45

Leu Gly Asn Ser Leu Val Ile Thr Val Leu Ala Arg Ser Lys Pro Gly  
 50 55 60

Lys Pro Arg Ser Thr Thr Asn Leu Phe Ile Leu Asn Leu Ser Ile Ala  
 65 70 75 80

Asp Leu Ala Tyr Leu Leu Phe Cys Ile Pro Phe Gln Ala Thr Val Tyr  
                     85                    90                    95  
 Ala Leu Pro Thr Trp Val Leu Gly Ala Phe Ile Cys Lys Phe Ile His  
                     100                    105                    110  
 Tyr Phe Phe Thr Val Ser Met Leu Val Ser Ile Phe Thr Leu Ala Ala  
                     115                    120                    125  
 Met Ser Val Asp Arg Tyr Val Ala Ile Val His Ser Arg Arg Ser Ser  
                     130                    135                    140  
 Ser Leu Arg Val Ser Arg Asn Ala Leu Leu Gly Val Gly Phe Ile Trp  
                     145                    150                    155                    160  
 Ala Leu Ser Ile Ala Met Ala Ser Pro Val Ala Tyr His Gln Arg Leu  
                     165                    170                    175  
 Phe His Arg Asp Ser Asn Gln Thr Phe Cys Trp Glu Gln Trp Pro Asn  
                     180                    185                    190  
 Lys Leu His Lys Lys Ala Tyr Val Val Cys Thr Phe Val Phe Gly Tyr  
                     195                    200                    205  
 Leu Leu Pro Leu Leu Leu Ile Cys Phe Cys Tyr Ala Lys Val Leu Asn  
                     210                    215                    220  
 His Leu His Lys Lys Leu Lys Asn Met Ser Lys Lys Ser Glu Ala Ser  
                     225                    230                    235                    240  
 Lys Lys Lys Thr Ala Gln Thr Val Leu Val Val Val Val Val Phe Gly  
                     245                    250                    255  
 Ile Ser Trp Leu Pro His His Val Val His Leu Trp Ala Glu Phe Gly  
                     260                    265                    270  
 Ala Phe Pro Leu Thr Pro Ala Ser Phe Phe Phe Arg Ile Thr Ala His  
                     275                    280                    285  
 Cys Leu Ala Tyr Ser Asn Ser Ser Val Asn Pro Ile Ile Tyr Ala Phe  
                     290                    295                    300  
 Leu Ser Glu Asn Phe Arg Lys Ala Tyr Lys Gln Val Phe Lys Cys His  
                     305                    310                    315                    320  
 Val Cys Asp Glu Ser Pro Arg Ser Glu Thr Lys Glu Asn Lys Ser Arg  
                     325                    330                    335  
 Met Asp Thr Pro Pro Ser Thr Asn Cys Thr His Val  
                     340                    345

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1044 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATGGAAGTGG CTATGGTGAA CCTCAGTGAA GGGAAATGGGA GCGACCCAGA GCCGCCAGCC 60  
 CCGGAGTCCA GGCCGCTCTT CGGCATTGGC GTGGAGAACT TCATTACGCT GGTAGTGTTT 120  
 GGCCTGATTT TCGCGATGGG CGTGCTGGGC AACAGCCTGG TGATCACCGT GCTGGCGCGC 180  
 AGCAAACCAG GCAACCCCCG CAGCACCACC AACCTGTTTA TCCTCAATCT GAGCATCGCA 240  
 GACCTGGCCT ACCTGCTCTT CTGCATCCCT TTTCAGGCCA CCGTGTATGC ACTGCCCACC 300  
 TGGGTGCTGG GCGCCTTCAT CTGCAAGTTT ATACACTACT TCTTCACCGT GTCCATGCTG 360  
 GTGAGCATCT TCACCCTGGC CGCGATGTCT GTGGATCGCT ACGTGGCCAT TGTGCACTCG 420  
 CGGCGCTCCT CCTCCCTCAG GGTGTCCCGC AACGCACTGC TGGGCGTGGG CTTCATCTGG 480  
 GCGCTGTCCA TCGCCATGGC CTCGCCGGTG GCCTACCACC AGCGTCTTTT CCATCGGGAC 540  
 AGCAACCAGA CTTTCTGCTG GGAGCAGTGG CCCAACAAAGC TCCACAAGAA GGCTTACGTG 600  
 GTGTGCACTT TCGTCTTTGG GTACCTTCTG CCCTTACTGC TCATCTGCTT TTGCTATGCC 660  
 AAGGTCCTTA ATCATCTGCA TAAAAAGCTG AAAAACATGT CAAAAAAGTC TGAAGCATCC 720  
 AAGAAAAAGA CTGCACAGAC CGTCCTGGTG GTCGTTGTAG TATTTGGCAT ATCCTGGCTG 780  
 CCCCATCATG TCGTCCACCT CTGGGCTGAG TTTGGAGCCT TCCCACTGAC GCCAGCTTCC 840  
 TTCTTCTTCA GAATCACCGC CCATTGCCTG GCATACAGCA ACTCCTCAGT GAACCCCATC 900  
 ATATATGCCT TTCTCTCAGA AAACTTCCGG AAGGCGTACA AGCAAGTGTT CAAGTGTCAT 960  
 GTTTGCGATG AATCTCCACG CAGTGAAACT AAGGAAAACA AGAGCCGGAT GGACACCCCG 1020  
 CCATCCACCA ACTGCACCCA CGTG 1044

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Leu Leu Thr Leu His Pro Val Trp Ser Gln Lys His Arg Thr Ser His  
 1 5 10 15  
 Trp Ala Ser Arg Val Val Leu Gly Val Trp Leu Ser Ala Thr Ala Phe  
 20 25 30  
 Ser Val Pro Tyr Leu Val Phe Arg Glu Thr Tyr Asp Asp Arg Lys Gly  
 35 40 45  
 Arg Val Thr Cys Arg Asn Asn Tyr Ala Val Ser Thr Asp Trp Glu Ser  
 50 55 60  
 Lys Glu Met Gln Thr Val Arg Gln Trp Ile His Ala Thr Cys Phe Ile  
 65 70 75 80  
 Ser Arg Phe Ile Leu Gly Phe Leu Leu Pro Phe Leu Val Ile Gly Phe  
 85 90 95  
 Cys Tyr Glu Arg Val Ala Arg Lys Met Lys Glu Arg Gly Leu Phe Lys  
 100 105 110  
 Ser Ser Lys Pro Phe Lys Val Thr Met Thr Ala Val Ile  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTTCTCACCC TTCACCCAGT GTGGTCCCAA AAGCACCGAA CCTCACACTG GGCTTCCAGA 60  
 GTCGTTCTGG GAGTCTGGCT CTCTGCCACT GCCTTCAGCG TGCCCTATTT GGTTTTCAGG 120  
 GAGACATATG ATGACCGTAA AGGAAGAGTG ACCTGCAGAA ATAACCTACGC TGTGTCCACT 180  
 GACTGGGAAA GCAAAGAGAT GCAAACAGTA AGACAATGGA TTCATGCCAC CTGTTTCATC 240  
 AGCCGCTTCA TACTGGGCTT CCTTCTGCCT TTCTTAGTCA TTGGCTTTTG TTATGAAAGA 300  
 GTAGCCCGCA AGATGAAAGA GAGGGGCCTC TTAAATCCA GCAAACCCTT CAAAGTCACG 360  
 ATGACTGCTG TTATCTC 377

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Phe Lys Ile Val Lys Pro Leu Ser Thr Ser Phe Ile Gln Ser Val Asn  
 1 5 10 15  
 Tyr Ser Lys Leu Val Ser Leu Val Val Trp Leu Leu Met Leu Leu Leu  
 20 25 30  
 Ala Val Pro Asn Val Ile Leu Thr Asn Gln Arg Val Lys Asp Val Thr  
 35 40 45  
 Gln Ile Lys Cys Met Glu Leu Lys Asn Glu Leu Gly Arg Gln Trp His  
 50 55 60  
 Lys Ala Ser Asn Tyr Ile Phe Val Gly Ile Phe Trp Leu Val Phe Leu  
 65 70 75 80  
 Leu Leu Ile Ile Phe Tyr Thr Ala Ile Thr Arg Lys Ile Phe Lys Ser  
 85 90 95  
 His Leu Lys Ser Arg Lys Asn Ser Ile Ser Val Lys Lys Lys Ser Ser  
 100 105 110  
 Arg Asn Ile Phe Ser Ile Val  
 115

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTCAAGATTG TGAAGCCCCT TTCCACGTCC TTCATCCAGT CTGTGAACTA CAGCAAACCTC 60  
 GTCTCGCTGG TGGTCTGGTT GCTCATGCTC CTCCTCGCCG TCCCCAACGT CATTCTCACC 120

AACCAGAGAG TTAAGGACGT GACGCAGATA AAATGCATGG AACTTAAAAA CGAACTGGGC 180  
 CGCCAGTGGC ACAAGGCGTC AAACTACATC TTTGTGGGCA TTTTCTGGCT TGTGTTTCCTT 240  
 TTGCTAATCA TTTTCTACAC TGCTATCACC AGGAAAATCT TTAAGTCCCA CCTGAAATCC 300  
 AGAAAGAATT CCATCTCGGT CAAAAAGAAA TCTAGCCGCA ACATCTTCAG CATCGTG 357

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Val Asp Leu Leu Ala Ala Leu Thr Leu Met Pro Leu Ala Met Leu Ser  
 1 5 10 15  
 Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly Glu Val Ala Cys Arg  
 20 25 30  
 Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu Ala Ile Leu Ser  
 35 40 45  
 Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Tyr Val Val His Pro Met  
 50 55 60  
 Arg Tyr Glu Val Arg Met Lys Leu Gly Leu Val Ala Ser Val Leu Val  
 65 70 75 80  
 Gly Val Trp Val Lys Ala Leu Ala Met Ala Ser Val Pro Val Leu Gly  
 85 90 95  
 Arg Val Ser Trp Glu Glu Gly Pro Pro Ser Val Pro Pro Gly Cys Ser  
 100 105 110  
 Leu Gln Trp Ser His Ser Ala Tyr Cys Gln Leu Phe Val Val Val Phe  
 115 120 125  
 Ala Val Leu Tyr Phe Leu Leu Pro Leu Leu Leu Ile Leu Val Val Tyr  
 130 135 140  
 Cys Ser Met Phe Arg Val Ala Arg Val Ala Ala Met Gln His Gly Pro  
 145 150 155 160  
 Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg Ser Glu Ser Leu Ser  
 165 170 175

Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro Gln Thr Thr Pro  
                   180                  185                  190

His Arg Thr Phe Gly Gly Gly Lys Ala Ala Val Val Leu Leu Ala Val  
                   195                  200                  205

Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe Ser Phe His Leu  
           210                  215                  220

Tyr Val Ala Leu Ser Ala Gln Pro Ile Ala Ala Gly Gln Val Glu Asn  
   225                  230                  235                  240

Val Val Thr Trp Ile Gly Tyr Phe Cys Phe Thr Ser  
                   245                  250

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 756 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GTGGACCTGC TGGCTGCCCT GACCCTCATG CCTCTGGCCA TGCTCTCCAG CTCCGCCCTC 60

TTTGACCACG CCCTCTTTGG GGAGGTGGCC TGCCGCCTCT ACTTGTTTCCT GAGCGTCTGC 120

TTTGTGAGCC TGGCCATCCT CTCGGTGTCC GCCATCAATG TGGAGCGCTA CTATTATGTG 180

GTCCACCCCA TGCCTATGA GGTGCGCATG AACTGGGGC TGGTGGCCTC TGTGCTGGTG 240

GGCGTGTGGG TGAAGGCCCT GGCCATGGCT TCTGTGCCAG TGTTGGGAAG GGTGTCCTGG 300

GAGGAAGGCC CTCCCAGTGT CCCCCAGGC TGTTCACTCC AATGGAGCCA CAGTGCCTAC 360

TGCCAGCTTT TCGTGGTGGT CTTGCGCGTC CTCTACTTCC TGCTGCCCCCT GCTCCTCATC 420

CTTGTGGTCT ACTGCAGCAT GTTCCGGGTG GCTCGTGTGG CTGCCATGCA GCACGGGCCG 480

CTGCCCACGT GGATGGAGAC GCCCCGGCAA CGCTCCGAGT CTCTCAGCAG CCGCTCCACT 540

ATGGTCACCA GCTCGGGGGC CCCGAGACC ACCCCTCACC GGACGTTTGG CGGAGGGAAG 600

GCAGCAGTGG TCCTCCTGGC TGTGGGAGGA CAGTTCCTGC TCTGTTGGTT GCCCTACTTC 660

TCCTTCCACC TCTATGTGGC CCTGAGCGCT CAGCCCATTG CAGCGGGGCA GGTGGAGAAC 720

GTGGTGACCT GGATTGGCTA CTTCTGCTTC ACCTCC 756

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Ala Asp Val Leu Val Thr Ala Ile Cys Leu Pro Ala Ser Leu Leu Val  
 1 5 10 15

Asp Ile Thr Glu Ser Trp Leu Phe Gly His Ala Leu Cys Lys Val Ile  
 20 25 30

Pro Tyr Leu Gln Ala Val Ser Val Ser Val Val Val Leu Thr Leu Ser  
 35 40 45

Ser Ile Ala Leu Asp Arg Trp Tyr Ala Ile Cys His Pro Leu Leu Phe  
 50 55 60

Lys Ser Thr Ala Arg Arg Ala Arg Gly Ser Ile Leu Gly Ile Trp Ala  
 65 70 75 80

Val Ser Leu Ala Val Met Val Pro Gln Ala Ala Val Met Glu Cys Ser  
 85 90 95

Ser Val Leu Pro Glu Leu Ala Asn Arg Thr Arg Leu Leu Ser Val Cys  
 100 105 110

Asp Glu Arg Trp Ala Asp Asp Leu Tyr Pro Lys Ile Tyr His Ser Cys  
 115 120 125

Phe Phe Ile Val Thr Tyr Leu Ala Pro Leu Gly Leu Met Ala Met Ala  
 130 135 140

Tyr Phe Gln Ile Phe Arg Lys Leu Trp Gly Arg Gln Ile Pro Gly Thr  
 145 150 155 160

Thr Ser Ala Leu Val Arg Asn Trp Lys Arg Pro Ser Asp Gln Leu Asp  
 165 170 175

Asp Gln Gly Gln Gly Leu Ser Ser Glu Pro Gln Pro Arg Ala Arg Ala  
 180 185 190

Phe Leu Ala Glu Val Lys Gln Met Arg Ala Arg Arg Lys Thr Ala Lys  
 195 200 205

Met Leu Met Val Val Leu Leu Val Phe Ala Leu Cys Tyr Leu Pro Ile

E1



210	215	220
Ser Val Leu Asn Val Leu Lys Arg Val Phe Gly Met Phe Arg Gln Ala		
225	230	235 240
Ser Asp Arg Glu Ala Ile Tyr Ala Cys Phe Thr Phe Ser His Trp Leu		
	245	250 255
Val Tyr Ala Asn Ser Ala Ala		
	260	

## (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 789 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

E1

GCCGATGTGC TGGTGACAGC CATCTGCCTG CCGGCCAGTC TGCTGGTAGA CATCACGGAA	60
TCCTGGCTCT TTGGCCATGC CCTCTGCAAG GTCATCCCCT ATCTACAGGC CGTGTCCTGT	120
TCAGTGGTCG TGCTGACTCT CAGCTCCATC GCCCTGGACC GCTGGTACGC CATCTGCCAC	180
CCGCTGTTGT TCAAGAGCAC TGCCCGGCGC GCCCGGGCT CCATCCTCGG CATCTGGGCG	240
GTGTCGCTGG CTGTCATGGT GCCTCAGGCT GCTGTCATGG AGTGTAGCAG CGTGCTGCCC	300
GAGCTGGCCA ACCGCACCCG CCTCCTGTCT GTCTGTGATG AGCGCTGGGC AGACGACCTG	360
TACCCCAAGA TCTACCACAG CTGCTTCTTC ATTGTCACCT ACCTGGCCCC ACTGGGCCTC	420
ATGGCCATGG CCTATTTCCA GATCTTCCGC AAGCTCTGGG GCCGCCAGAT CCCCAGCACC	480
ACCTCGGCCC TGGTGCGCAA CTGGAAGCGG CCCTCAGACC AGCTGGACGA CCAGGGCCAG	540
GGCCTGAGCT CAGAGCCCCA GCCCCGGGCC CGCGCCTTCC TGGCCGAGGT GAAACAGATG	600
CGAGCCCGGA GGAAGACGGC CAAGATGCTG ATGGTGGTGC TGCTGGTCTT CGCCCTCTGC	660
TACCTGCCCC TCAGTGTCTT CAACGTCCTC AAGAGGGTCT TCGGGATGTT CCGCCAAGCC	720
AGCGACCGAG AGGCCATCTA CGCCTGCTTC ACCTTCTCCC ACTGGCTGGT GTACGCCAAC	780
AGCGCCGCC	789

## (2) INFORMATION FOR SEQ ID NO:56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Glu Trp Asp Asn Gly Thr Gly Gln Ala Leu Gly Leu Pro Pro Thr  
 1 5 10 15  
 Thr Cys Val Tyr Arg Glu Asn Phe Lys Gln Leu Leu Leu Pro Pro Val  
 20 25 30  
 Tyr Ser Ala Val Leu Ala Ala Gly Leu Pro Leu Asn Ile Cys Val Ile  
 35 40 45  
 Thr Gln Ile Cys Thr Ser Arg Arg Ala Leu Thr Arg Thr Ala Val Tyr  
 50 55 60  
 Thr Leu Asn Leu Ala Leu Ala Asp Leu Leu Tyr Ala Cys Ser Leu Pro  
 65 70 75 80  
 E1 Leu Leu Ile Tyr Asn Tyr Ala Gln Gly Asp His Trp Pro Phe Gly Asp  
 85 90 95  
 Phe Ala Cys Arg Leu Val Arg Phe Leu Phe Tyr Ala Asn Leu His Gly  
 100 105 110  
 Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly Ile  
 115 120 125  
 Cys His Pro Leu Ala Pro Trp His Lys Arg Gly Gly Arg Arg Ala Ala  
 130 135 140  
 Trp Leu Val Cys Val Thr Val Trp Leu Ala Val Thr Thr Gln Cys Leu  
 145 150 155 160  
 Pro Thr Ala Ile Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val  
 165 170 175  
 Cys Tyr Asp Leu Ser Pro Pro Ala Leu Ala Thr His Tyr Met Pro Tyr  
 180 185 190  
 Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ala Ala Leu  
 195 200 205  
 Leu Ala Cys Tyr Cys Leu Leu Ala Cys Arg Leu Cys Arg Gln Asp Gly  
 210 215 220  
 Pro Ala Glu Pro Val Ala Gln Glu Arg Arg Gly Lys Ala Ala Arg Met

225                      230                      235                      240  
 Ala Val Val Val Ala Ala Ala Phe Ala Ile Ser Phe Leu Pro Phe His  
                                  245                      250                      255  
 Ile Thr Lys Thr Ala Tyr Leu Ala Val Gly Ser Thr Pro Gly Val Pro  
                                  260                      265                      270  
 Cys Thr Val Leu Glu Ala Phe Ala Ala Ala Tyr Lys Gly Thr Arg Pro  
                                  275                      280                      285  
 Phe Ala Ser Ala Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe Thr  
                                  290                      295                      300  
 Gln Lys Lys Phe Arg Arg Arg Pro His Glu Leu Leu Gln Lys Leu Thr  
 305                      310                      315                      320  
 Ala Lys Trp Gln Arg Gln Gly Arg  
                                  325

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 984 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ATGGAATGGG ACAATGGCAC AGGCCAGGCT CTGGGCTTGC CACCCACCAC CTGTGTCTAC                      60  
 CGCGAGAACT TCAAGCAACT GCTGCTGCCA CCTGTGTATT CGGCGGTGCT GCGGGCTGGC                      120  
 CTGCCGCTGA ACATCTGTGT CATTACCCAG ATCTGCACGT CCCGCCGGGC CCTGACCCGC                      180  
 ACGGCCGTGT ACACCCTAAA CCTTGCTCTG GCTGACCTGC TATATGCCTG CTCCCTGCCC                      240  
 CTGCTCATCT ACAACTATGC CCAAGGTGAT CACTGGCCCT TTGGCGACTT CGCCTGCCGC                      300  
 CTGGTCCGCT TCCTCTTCTA TGCCAACCTG CACGGCAGCA TCCTCTTCCT CACCTGCATC                      360  
 AGCTTCCAGC GCTACCTGGG CATCTGCCAC CCGCTGGCCC CCTGGCACAA ACGTGGGGGC                      420  
 CGCCGGGCTG CCTGGCTAGT GTGTGTAACC GTGTGGCTGG CCGTGACAAC CCAGTGCCTG                      480  
 CCCACAGCCA TCTTCGCTGC CACAGGCATC CAGCGTAACC GCACTGTCTG CTATGACCTC                      540  
 AGCCCGCCTG CCCTGGCCAC CCACTATATG CCCTATGGCA TGGCTCTCAC TGTCATCGGC                      600  
 TTCCTGCTGC CCTTTGCTGC CCTGCTGGCC TGCTACTGTC TCCTGGCCTG CCGCCTGTGC                      660

CGCCAGGATG GCCCGGCAGA GCCTGTGGCC CAGGAGCGGC GTGGCAAGGC GGGCCGCATG	720
GCCGTGGTGG TGGCTGCTGC CTTTGCCATC AGCTTCCTGC CTTTTCACAT CACCAAGACA	780
GCCTACCTGG CAGTGGGCTC GACGCCGGGC GTCCCCTGCA CTGTATTGGA GGCCTTTGCA	840
GCGGCCTACA AAGGCACGCG GCCGTTTGCC AGTGCCAACA GCGTGCTGGA CCCCATCCTC	900
TTCTACTTCA CCCAGAAGAA GTTCCGCCGG CGACCACATG AGCTCCTACA GAAACTCACA	960
GCCAAATGGC AGAGGCAGGG TCGC	984

## (2) INFORMATION FOR SEQ ID NO:58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGCCATCT TCGCTGCCAC AGGCAT 26

## (2) INFORMATION FOR SEQ ID NO:59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AGACAGTAGC AGGCCAGCAG GGCAGCAAA 29

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D) OTHER INFORMATION: /note= N is inosine; Y is C or T; S is G or C;  
K is G or T; M is A or C."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CTGTGYGYSA TYGCNNTKGA YMGSTAC

27

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

((ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(D) OTHER INFORMATION: /note= N is inosine; S is G or C; W is A or T;  
R is A or G; K is G or T; Y is C or T."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AKGWAGWAGG GCAGCCAGCA GANSRYGAA

29